

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 00:17:03 ; Search time 2461.04 seconds

(without alignments)
10930.628 Million cell updates/sec

Title: US-09-001-737-7

Perfect score: 1661
Sequence: 1 GAATTCGGCTCATATGCA.....TGGCGGATAGCCGATTC 1661

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_esthm:*
16: em_estom:*
17: gb_ges8:*
18: em_ges8_hum:*
19: em_ges8_inv:*
20: em_ges8_pln:*
21: em_ges8_vit:*
22: em_ges8_fun:*
23: em_ges8_mam:*
24: em_ges8_mus:*
25: em_ges8_other:*
26: em_ges8_pro:*
27: em_ges8_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	472	28.4	2265	11	AY109623
2	431.4	26.0	2290	11	AY104969
3	430.6	25.9	2338	11	AY103778
4	414.2	24.9	1327	17	BH770613
5	383.6	23.1	2143	11	AY108560
6	302.8	18.2	1376	11	AY106465

7	290	17.5	1387	11	AY108518
8	263.2	15.8	887	17	CNS074DM
9	262.8	15.8	1090	14	BW799922
10	261.8	15.8	878	12	BF275584
11	257.2	15.5	1035	9	AL518632
12	254	15.3	977	12	BC321293
13	253.4	15.3	988	9	AL532233
14	251.6	15.1	955	9	AL515262
15	249.6	15.0	1017	9	AL515579
16	249	15.0	877	13	BF926411
17	248.6	15.0	810	12	BF627437
18	248	14.9	959	9	AL557150
19	247	14.9	746	14	BU003474
20	246.4	14.8	980	9	AL557181
21	245	14.8	765	14	BO967621
22	243	14.6	645	10	AM224051
23	242	14.6	633	14	BU014013
24	239.4	14.4	716	14	DA6006
25	237.6	14.3	637	10	AM223768
26	237.6	14.3	1119	13	BM458421
27	236.2	14.2	668	10	AM398404
28	233	14.0	771	12	BF617440
29	231.2	13.9	677	10	AV938920
30	230.2	13.9	698	14	BO860576
31	229.6	13.8	1051	13	BM478208
32	228.8	13.8	744	14	BU000648
33	227.4	13.7	680	10	AM330455
34	227.2	13.7	632	12	BG128308
35	226.6	13.6	650	9	AC432272
36	226	13.6	790	12	BC599254
37	226	13.6	1351	10	BE422296
38	225.6	13.6	895	14	BO216655
39	225.4	13.6	946	14	BO882339
40	225.2	13.6	709	9	AT486676
41	224.8	13.5	1016	13	BM450130
42	224.8	13.5	739	14	BO915279
43	223	13.4	744	13	BT176450
44	222.4	13.4	654	13	BT176456
45	222.4	13.4	825	10	BE642158

ALIGNMENTS

RESULT 1
AY109623
LOCUS 2265 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays CL2221_1 mRNA sequence.
ACCESSION AY109623
VERSION AY109623.1 GI:21213414
KEYWORDS
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 2265)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitelitt, M.S.,
Arthur, L.M., Hanley, M., Morgan, M. and Finney, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes (2002)
Unpublished (2002)
REFERENCE
2 (bases 1 to 2265)
Coe, E.C.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
LOCATION/Qualifiers
1. 2265
/organism="Zea mays"
/db_xref="MaizeDB:630867"
/db_xref="taxon:4577"
/clone="CL2221_1"

Query Match	28.48;	Score 472;	DB 11;	Length 2265;
Best Local Similarity	56.48;	Pred. No. 1.3e-120;		
Matches 913; Conservative	0;	Mismatches 697;	Indels 9;	Gaps 31

Db	1128	TTGGGGAAAACAGAGAGCGCAACTTACAGACAGCTTGCAGATCCTTACTGAGAGAGAGCTAA	1187
Oy	910	TTACGAGAGATCTTAGAGACTTAATTAAGAATGCTACAAATGACAGCCTTGGACAGCGTG	969
Db	1188	TAACTGAGAGACTAGSAGATGACCTTGAGAAATTTTGAAGCTCACATGCTGGGATCATGCGN	1247
Oy	970	CTACAAATTAACAGTTGATTAAGATATGCACAGTAAATTTGTAAGGTTCCAGAAATTCAGAG	1039
Db	1248	NNNNNGTACGTCTCTTAAGATGATACAGTGTATTTCTTGTATGTGAGCCGAGACAGAAAGT	1307
Oy	1030	CTATTGCTAACCGTATTTGCTACTGATTAATTCGCAATTAGAAACCAACTTCTGACTTGG	1089
Db	1308	CCATTGAGAGAGAGGCGCAGAGAGATTAATGATAGCAAGATTTGAGATAGCACTTCAGATTAAG	1367
Oy	1090	ACCGTGAAGAAACTACAGAAACGTTTGTGGCCAAATTAAGTGGTGGTGTACCTGTATACAAAG	1149
Db	1368	ATTAAGGAAAAGCTCCAGAGAGCGGTGTGGCAAGGCTCTCTGAGAGTGTCTGTCTTCTGAGAA	1427
Oy	1150	TAGAGAGCTCCACAGACAGACAGCTTTAAAGAAATGAATCAATCGCATTTAGATAGCTCTAA	1209
Db	1428	TTGGAGAGAGCAGCAGCAGCAAGAGTTGTGAGAAAGAAAGATAGATGACAGATGACATGA	1487
Oy	1210	ATGCTACAGCTGACCCGCTTGAAGAGATATGCTGTGGTGTGTGAAACAGCACTATATA	1269
Db	1488	ATGCTACTAAGAGCTCTGTGTAAGAGGATATTGACAGAGTGATGACAGGTGTGTGTCTCTCT	1547
Oy	1270	CGGTATTTGAAAAGATGACAGACCTTGTGAGCTTG---AGGCGATATGATGATACAGAGCTA	1326
Db	1548	ATGATCATGAGAGAGCGTTGATTAATTCAGACAGAGCAAGCTTCATATAGAAATTTGGTGGC	1607
Oy	1327	ACATTGTGCTGTGCTCTGTGAAGAGACCGTACGTCGCTCAATTCCTTAATCTGGGTACG	1386
Db	1608	AAATCATTTACGAATCCTTTGAAACACCTGTACACACATTTCCCTCAAAATGCTGGGGTGG	1667
Oy	1387	TAGGCTCCGATATTTTGTAGACAG---TTGAAAACAGACCCCTGACAGAACAGATTTAATG	1443
Db	1668	AGGAGAGAGTATGTATGAGAAACCTTTTGGAGCAGAAATAATACGACTGGGTTATGATG	1727
Oy	1444	CTGCAAGAGGTATGAGGTTGATATGATATTAACAGAGATCAATTGACCTGTCTAAAGTAA	1503
Db	1728	CTGCTAAAGGTATATTTGATATGTAAGACCCGGTATATGACCCGCTAAAGGTTA	1787
Oy	1504	CACGATACGCGCTTAATAATGACGCTTCTGTAGCTAGTCTTATTTTGAACAAGAGACAG	1563
Db	1788	TCAGAAATGCTTTGTGTGATGCTGCTAGTGTGTGTCTGTATGACAAACGAGGATATCA	1847
Oy	1564	TTTGTGCTAATTAACCTGAACGAGTACGACGCCAGCGCCAGCAANTGCCAGAGATGAT	1622
Db	1848	TAAATTGATGAGATTTCCAGAGAGAGGACGACCGGCTCAGCAATAGGATGGCGCATGGGT	1906
RESULT 2			
LOCUS	AY104969	2290 bp	mRNA linear .HTC 25-MAY-2002
DEFINITION	2ea mays PC0070942 mRNA sequence.		
ACCESSION	AY104969		
VERSION	AY104969.1	GI:2108047	
KEYWORDS	HTC.		
SOURCE	2ea mays.		
ORGANISM	2ea mays.		
REFERENCE			
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Rosaceae; PRNC		
TITLE	1 (bases 1 to 2290)		
	Halevy,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,		
	Arthur,I.W., Hanley,M., Morgante,M. and Tingey,S.V.		
	Maize Mapping Project/DuPont Consensus Sequences for Design of		
	Overgo Ribprobes		
	Unpublished (2002)		
	2 (bases 1 to 2290)		
	Coe,E.C.		
	Direct Submission		
JOURNAL	Submitted (25-Apr-2002)		
TITLE	Maize Mapping Project, University of		

FEATURES
source
1. 2290
/organism="Zea mays"
/db_xref="maize:633867"
/db_xref="taxon:457"
/clone="PC070942"
/clone_id="Maize Mapping Project/Dupont Consensus Library"

BASE COUNT 684 a 457 c 583 g 565 t 1 others
ORIGIN
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

Query Match 26.08; Score 431.4; DB 11; Length 2290;
Best Local Similarity 57.98; Pred No 3.1e-109;
Matches 883; Conservative 0; Mismatches 622; Indels 19; Gaps 6;

QY 56 GGAGTGTATCTTTCAGATACCTGCAAGTAAAGCTTGTCTTAAAGGCGCAATGTT 125
DB 426 GGAGTCAACAGCTTGCAGATCTGCGGGTTCCTTGTGACCAAGGCGCAATGTA 485
QY 126 GTTCTTAAAAAGCTTTGGTTCCTCTTAATTAATGACGGGGTAACTTGTCTAA 185
DB 486 GTCTCGAAGCAAGTATGCTGCTCACTAAATGATGATGCTGCTGCTGCAAG 545
QY 186 GAGATCGAATTAGAAATCATTTTGAAGCAATGGGCAAAATGGTGTGAAAGGCT 245
DB 546 GAGGTGAACTGAGAGCCCTGTTAAATATGCTGCTAAATGCTCCGCAAGCTGCT 605
QY 246 TCTAAACATGATATGCTGCTGATGGGAGCACTGCAACAGTTTGAACAGAGC 305
DB 606 GCTAAACAAATGACTGCTGCTGCTGATGGAGCAACCTGCTGCTGCTGCAAGG 665
QY 306 ATGTGTCATGAAGGACATAAAATGAGACAGGAGCTTAACTTAACTGATTCCTG 365
DB 666 ATGATCTAGAGGCTTAAAGGTTGAGTGTGCTGCTTAACTGATTCAGATCACCT 725
QY 366 GGCATTGAAGCAAGCAAGCAAGCTGTGAACCTTGAAGCCATTGCTCAACTGTA 425
DB 726 GGTATTGAGAAACAGCAAGCAAGCTGATGATCACTCAAAAGATGCTCAAGGAGT 785
QY 426 TCTGCAAGAAAGCTATTTGCTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 482
DB 786 TGAGGACAGTGAAG--TTGCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
QY 483 GGAGAGTATATCTCAGAAAGCTATGAGAGCTGTGGGCAAGAGTGTGATTAACATG 542
DB 844 GGGATATATGATAGCTGAGGCTATGAAAAAGGTTGGCGGAGGAGGCTGACACAT 903
QY 543 GAATCTGAGATGATGAAGCAAGCTTGAAGTGTGAGAGGATGATTTGAGCGTGT 602
DB 904 GAAGGAAAGAGTGTGAAATTAACCTGATTCCTGTTGAGGAAAGTCAAGTGTGCG 963
QY 603 TACCTGCTCATATGATGCTGACAGCAAGCAAGAAATGAGGAGCTTGAAGCAAC 662
DB 964 TATATTTCTCCCTACTGTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1023
QY 663 TTTATCTTAATCAGGATAAAAAGTGTCAACATCCAGACATTTGGCCTACTTGG 722
DB 1024 AAGCTTCTCTGTGAGCAAGAAATTAACAAAGCTGAGATCTTATCACTTCTGAG 1083
QY 723 GAAGTCTTAAACCAAGCTGCTTACTTACTTATTTAGTGTGATGATGATGATGAT 782
DB 1084 GATGCTATTAGAGTGTGATTCATTTAATAGTGTGAGGAGGAGGAGGAGGAGG 1143
QY 783 CTTCACACCTTGTCTGAAAGAAAGTGTGATGATTTTAAATGATGATGATGATG 842
DB 1144 CTTCACACCTTGTGATTAATGCTTGAAGGAGTGTGATGATGATGATGATGATG 1203

QY 843 CCAGATTTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
DB 1204 CCGTGTGTTGAGAGGCGCAAAAGTCAATATCTGATGATGATGATGATGATGATG 1263
QY 903 ACAGTATTAACAGGATCTAGAGCTTGAATTAAGATGCTTAAAGTACAGGAGGAG 962
DB 1264 ACTGCTATCAGAGAAAGTGTGATTAATCTTGAAGAGGAGGAGGAGGAGGAGG 1323
QY 963 CAGGCTGCTAAGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGT 1022
DB 1324 ACTGCTGCTAAGGTTGATGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGT 1383
QY 1023 TCAAGAGCTATGCTTAAAGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1082
DB 1384 CAGAGAGAGTAAACAAAGGCTGACACAAATCAAGATGATGATGATGATGATG 1443
QY 1083 GACTTGACCGTGAAGAACTTACAGAGAGCTTTAAAGAAATGAATGCTGCTGAT 1142
DB 1444 GAATATGAGAGAGAAAGAACTTAAACAGAGATGATGATGATGATGATGATGAT 1503
QY 1143 ATCAAGTATGAGAGCTTCAACAGAGAGCTTTAAAGAAATGAATGCTGCTGAT 1202
DB 1504 ATTCAGATGAG 1563
QY 1203 GCTCTAAATGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1262
DB 1564 GCGCTAAATGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1623
QY 1263 CTATATGAGGTTATTAAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1316
DB 1624 CTTTGAGGCTTGAATCAAAAGTATGATGATGATGATGATGATGATGATGATG 1683
QY 1317 AC---TGGAGCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1373
DB 1684 AAGGTTGAGGCTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1743
QY 1374 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1429
DB 1744 AATGCAAGCTTAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1803
QY 1430 AACAGATTTAATGCTGCAACAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1489
DB 1804 TATGGG-TTCAATGCGGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1862
QY 1490 CCCTGCTCAAGTAAACAGATCAGGCTTCAAAATGACCTTCTGATGATGATGAT 1549
DB 1863 TCCACCAAGAGTGTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1922
QY 1550 GACACAG 1573
DB 1923 CACCTGATGAG 1946

RESULT 3
LOCUS AY103778 2338 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays PC063180 mRNA sequence.
ACCESSION AY103778
VERSION AY103778.1 GI:21206856
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Hainey C.F., Dolan M., Miao G.H., Vogel J.M., Whittle M.S.,
Arthur L.W., Hanafey M., Morgante M. and Tingey S.V.
TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 2338)

AUTHORS Coe, E. C.
 TITLE Direct Submission
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
 FEATURES
 source Location/Qualifiers
 1..2338
 /organism="Zea mays"
 /db_xref="MaizeDB:633377"
 /db_xref="taxon:4577"
 /clone="PC0063180"
 /clone_lib="Maize Mapping Project/Dupont Cornsensus
 Library"

/note="this sequence is part of a project of EST
 assemblies resulting from the application of public
 contigs to seed Dupont contigs; this resource was
 assembled by Dupont as part of a collaboration for the
 overgo addressing of BACs in conjunction with the Maize
 Mapping Project"

BASE COUNT 668 a 483 c 643 g 544 t

Query Match 25.9% Score 430.6; DB 11: Length 2338;
 Best Local Similarity 56.2%; Pred. No. 5,2e-109;
 Matches 875; Conservative 0; Mismatches 689; Indels 13; Gaps 3;

Oy 66 GGAGTTGATAGTTACGATACCGTCAAGTACGCTTGGCTTAAGGCGCATGTT 125
 Db 452 GGAGTTGATAGTTACGATACCGTCAAGTACGCTTGGCTTAAGGCGCATGTT 125
 Oy 126 GTTCTGTAAGGCTTGTGCTCCCTTAATTACTAATGCGGGTAACCATTTGTA 185
 Db 512 GTTCTGTAAGGCTTGTGCTCCCTTAATTACTAATGCGGGTAACCATTTGTA 185
 Oy 186 GAGATGCAATTAAGATATTTTGAAGATGAGGAGCAAAATTTGGTGTGAGTGGT 245
 Db 572 GAGATGCAATTAAGATATTTTGAAGATGAGGAGCAAAATTTGGTGTGAGTGGT 245
 Oy 246 TCTAAGACCAATATTTGCTGTGATGAGGAGCAATGCTCAAGGTTTGAAGAGCC 305
 Db 632 TCTAAGACCAATATTTGCTGTGATGAGGAGCAATGCTCAAGGTTTGAAGAGCC 305
 Oy 306 ATTGTTCAAGGACTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 691
 Db 692 ATTGTTCAAGGACTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 691
 Oy 366 GCGATGGAACAGCAACAGCAAGCTGTTGAGGCTTGAAGGCAATTTGCTCAACTGTA 425
 Db 752 GCGATGGAACAGCAACAGCAAGCTGTTGAGGCTTGAAGGCAATTTGCTCAACTGTA 425
 Oy 426 TCTGCAAGAGCAATTTGCTGCAAGGCTGCTGCAAGTATCATACGCTTGAAAAAGTTGA 485
 Db 812 TCTGCAAGAGCAATTTGCTGCAAGGCTGCTGCAAGTATCATACGCTTGAAAAAGTTGA 485
 Oy 486 GAGTATATCTCAGAGCTATGAGCGCTGTGGCAACAGATGCTGATACCATCGAAGA 545
 Db 872 GAGTATATCTCAGAGCTATGAGCGCTGTGGCAACAGATGCTGATACCATCGAAGA 545
 Oy 546 TCTGAGGTATGGAAGCAAGTGAAGGTGTTGAGGAGGAGGAGGAGGAGGAGGAGG 931
 Db 932 TCTGAGGTATGGAAGCAAGTGAAGGTGTTGAGGAGGAGGAGGAGGAGGAGGAGG 931
 Oy 606 CTGCTCAATACAGTGTGACAGACAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 991
 Db 992 CTGCTCAATACAGTGTGACAGACAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 991
 Oy 992 ATCTCTCCGATCTTGTAAAGAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 1051
 Db 666 ATCTATATCGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 724
 Oy 1052 CTGCTTTGTTGATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1111
 Db 725 AGTCTTAAACCAACGCTGATTAATTTGAGATGATGATGATGATGATGATGATGATG 784
 Oy 1112 AGCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1171

Oy 785 TCCAACTGCTGCTTGAACAGATGCTGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 844
 Db 1172 TCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
 Oy 845 AGGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 904
 Db 1232 TGGTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1291
 Oy 905 AGTATATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 964
 Db 1292 TGTATATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1351
 Oy 965 GCGCT 1024
 Db 1352 AGCTGCAAGG 1411
 Oy 1025 AGAGCTATGCT 1084
 Db 1412 GGAAGAGG 1471
 Oy 1085 CTGTAAGCT 1144
 Db 1472 ATATGAG 1531
 Oy 1145 CAAAGTATGAGG 1204
 Db 1532 TCAGTATGAGG 1591
 Oy 1205 TCTAATGCT 1264
 Db 1592 CTTAATGCT 1651
 Oy 1265 TATTAAGG 1315
 Db 1652 TTTGCGGCT 1711
 Oy 1316 TACTGAGCT 1375
 Db 1712 GCTTGAAGGAG 1771
 Oy 1376 TGGTGGGAGG 1432
 Db 1772 TGGGAGG 1831
 Oy 1433 AGGATTTAATGCT 1492
 Db 1832 TGGTATCAATGCT 1891
 Oy 1493 TGTCAAGTATGCT 1552
 Db 1892 TACTAAGGAG 1951
 Oy 1553 AACAGAGCAATTTGCT 1609
 Db 1952 ATTGATGCT 2008

RESULT 4
 BH770613/c 1327 bp DNA linear GSS 01-MAY-2002
 LOCUS LMGt6372 MG1363 Random Sequence Tag Library Lactococcus lactis
 DEFINITION subsp. cremoris genomic, DNA sequence.
 ACCESION BH770613
 VERSION BH770613.1 GI:20373570
 KEYWORDS GSS.
 SOURCE Lactococcus lactis subsp. cremoris.
 ORGANISM Lactococcus lactis subsp. cremoris.
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Lactococcus.
 REFERENCE 1 (bases 1 to 1327)
 AUTHORS Bolotin, A., Ehrlich, S. D. and Sorokin, A.
 TITLE Studies of genomes of dairy bacteria Lactococcus lactis
 JOURNAL Sci. Aliments, (2002) in press

Db 571 GGCAATGTGGACATTAATCTTCAGGGGCAATTCAGTGTCCGTTAAGAGGCCATTGATTA 630
 Oy 377 AGCAACAGACAGAGCTGTGTAAGCCCTGTAAGCCATTCCTATCTGCGCAAGA 436
 Db 631 GACTGTTCAGAAATGCTGGAGCACTTGAGAAATATACAGCCGCTCAAGAGTAGTG 690
 Oy 437 AGCTATTGCTGAGCTGCTGAGTATCATCTACGCTGAGAAAGTTGGAGATAT---AT 493
 Db 691 GGATATTAAAGGTGTCTGCTCATATCAGCTGGAATATGTAATTTGTGGGACTATAT 750
 Oy 494 CTCAGAAAGCTATGGAGGCTGTGGGCAAGATGGTGGATATTCATTCAGAAATATTCGAG 553
 Db 751 CGCCGAAGCTATATGACAAAGTTGGCCGATGGTGGTCTCTCATATGAGTGCATGTC 810
 Oy 554 TATGGAAGAAGAACTGAAGTGTGAAGCAAGCAATTTGACCGTGTACCTGTCA 613
 Db 811 GTTGAAGACCACTGATGATTAAGATGAGAGTGGAGCTTGACAGAGATATATCTCCC 870
 Oy 614 ATACATGCTCACAGCAATGAAAAAGTTGTCAGACCTTGAAAAACCATTAATCTTAAT 673
 Db 871 TCAGTTGCTCACTAACCTTAAAAATCTATTGTGAGTTGCAAAAATCTCGATTTCTGT 930
 Oy 674 CACGGAATAAAAAGTGTCAAAACATCCAGACATTTTGCCTACTTGTAGAGAGTTCTTA 733
 Db 931 CACTGATCAAGAAATATCATGATTAAGAAATTAATCTCTGTTGGAGAGACAAACACA 990
 Oy 734 AACCAACCGCTCATTAATCTATTAATGAGATGATGATGATGAGACACTTCCAAACCT 793
 Db 991 GTTAAAGACCACTTCTTATTAATGAGAGATGTAATGAGCGAGCGCTGGCAACAT 1050
 Oy 794 TGTCTGGAACAAGATGCTGTACTTCAATGATGATGATGATGATGATGATGATGATGAT 853
 Db 1051 AGCTATTAACAAGCTTAGAGAAATTTTAAATGGTGTGATCAAGCTCTGCTGTGG 1110
 Oy 854 TGATCTGCTAAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 913
 Db 1111 TGAGAGCGCTAAAGCTTCTTCTGAGAGATGATGATGATGATGATGATGATGATGAT 1170
 Oy 914 AGAGATCTAGAGATTAATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 973
 Db 1171 CAAGATCTTGTCTACTAGTGGAGATGATGATGATGATGATGATGATGATGATGATGAT 1230
 Oy 974 GATTACAGTGTAAAGATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1033
 Db 1231 AGTTACAACTCAAGTCTCTGAGACACATTAATGATGATGATGATGATGATGATGAT 1290
 Oy 1034 TGCTAACGCTATGCTAGCTATTAATGATGATGATGATGATGATGATGATGATGATGAT 1093
 Db 1291 CCAAGGCGAAGATCGCGAGCTGAGAGAGAGCTTCTGACAGGAGCTGACATGATGAT 1350
 Oy 1094 TGAAGAACTACAGAAAGCTTGGGCAATTAAGTGTGATGATGATGATGATGATGATGAT 1153
 Db 1351 TGAGAAATGCGACAGAGAAATGCAAAAGCTTCTGATGATGATGATGATGATGATGAT 1410
 Oy 1154 AGCTCAACAGAGAGAGCTTAAAAAGAACTTGGCTGATGATGATGATGATGATGATGAT 1213
 Db 1411 AGCATGACAGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1470
 Oy 1214 TACAGCTGACAGCTGTAAGAAAGTATGATGATGATGATGATGATGATGATGATGATGAT 1273
 Db 1471 GACTTTGACCAATGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1530
 Oy 1274 TATGAAAAATGACAGCTTCTGAGCTTGAAGGCGATGATGATGATGATGATGATGATGAT 1324
 Db 1531 ATGACATTCCTACCGCTATATCAAGAGAGAGCTGATGATGATGATGATGATGATGATGAT 1590
 Oy 1325 TAACATTTGCTGTGCTCTAGAAAGAGCTGATGATGATGATGATGATGATGATGATGATGAT 1384
 Db 1591 TGATATCATATGAGAAAGCTTGTGGACAGCTGATGATGATGATGATGATGATGATGATGAT 1650
 Oy 1385 CGAAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1444
 Db 1651 GGAAGGTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1710

Oy 1445 TCACAGAGTGTAGTGGCTTATGATTAACAGAAATCATGACCTGTCAAGTAAAC 1504
 Db 1711 CATGGCGACACAGACGAGAACTGTGGAGGCTGTGATGACCTGTGCAAGATGAC 1770
 Oy 1505 AGCATGAGGCTCAAAATGAGCTTCTGATGATGATGATGATGATGATGATGATGATGAT 1564
 Db 1771 TAGTGGCGCTTCCAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1830
 Oy 1565 TGTGCTAATTAACCTGACAGAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1624
 Db 1831 GCTGTGAG 1890
 Oy 1625 AGCAATGATG 1634
 Db 1891 TTTCACCATG 1900
 RESULT 6
 AY106465 1376 bp mRNA Linear HTC 25-MAY-2002
 LOCUS
 DEFINITION Zea mays PC0128697 mRNA sequence.
 ACCESSION AY106465
 VERSION AY106465.1 GI:21209543
 KEYWORDS
 SOURCE
 ORGANISM
 Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 1376)
 Hainey, C.E., Dolan, M., Miao, G.H., Vogel, J.M., Whitesalt, M.S.,
 Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
 Maize Mapping Project/Dupont Consensus Sequences for Design of
 Overgo Probes
 Unpublished (2002)
 2 (bases 1 to 1376)
 Coe, E.C.
 Direct Submission
 Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
 Location/Qualifiers
 1..1376
 /organism="Zea mays"
 /db_xref="taxon:4577"
 /clone="PC0128697"
 /clone_11b="Maize Mapping Project/Dupont Consensus
 Library"
 /note="this sequence is part of a project of EST
 assemblies resulting from the application of public
 contigs to seed Dupont contigs; this resource was
 assembled by Dupont as part of a collaboration for the
 overgo addressing of BACS in conjunction with the Maize
 Mapping Project."

BASE COUNT 397 a 277 c 359 g 343 t
 ORIGIN
 Query Match 18.2% Score 302.8; DB 11; Length 1376;
 Best Local Similarity 55.7% Pred. No. 2.5e-73;
 Matches 621; Conservative 0; Mismatches 487; Indels 6; Gaps 2;

Oy 478 AAGTTGAGAGATATCTCAAGAGATGAGAGCTGTGGCAAGAGAGAGAGAGAGAGAGAGAG 537
 Db 23 AAATGAGAGATATATCAAAAGCCATGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 82
 Oy 538 TCGAAGAACTCGAGAGATGAG 597
 Db 83 TTGTTGATGCAAAACATTTGAG 142
 Oy 598 GTGTTACTGCTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 657
 Db 143 GAGATACATATCTCTTACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 202

Oy	658	ACCCATTATCTTAATCAGCGATATAAANAATGCTCAAAATCCAAAGACATTTGGCACTAC	717
Db	203	ACCCCTTATCTTATTCATCCATGCAGAAAGAAATCTCAAAATAGATATCTCCCTCCAGCAT	262
Oy	718	TTGAGGAAGTTCTTAANAACCAACCGTCCATCTCTCATATATATATGATGATGATGGTG	777
Db	263	TAAATAATTTATCAAGAAATGCGAAGCGCTCTTCATGTTGGCTGAGATATTGAAGAG	322
Oy	778	AAGCACTTCCACACCCTTGCTGTGAAGAAATTCGCGTACTTTCATATGTTGGTCTGTCA	837
Db	323	ATGCTCTGTCAATGCTTGTACTGAAACAGCATCGCTGACATCAAGGATATGCTGTCTGA	382
Oy	838	AAGCCCGAGATTTGCTGATCGCTGTAAAGCTATGCTGTGAAGCAATCTCATCTTGAAC	897
Db	383	AACTCTCGAGTTTGGTGGAAATATGAAGGCGACAATCATAGATGACATGCTGTATACG	442
Oy	898	GTGTGACAGTATTACAGAGATCTAGACATTTAAATTAAGATGCTCATATGACAGCCC	957
Db	443	GAGGAGAGATTATTACCGAGAGACCGCGCTCTGATCTTGGCAAAAGTCAATTAACAATAC	502
Oy	958	TTGGACAGCGCTCTAAGATTACATGTTGATTAAGATACAGATAATTTGTAGAGTTAC	1017
Db	503	TTGGCACTGCTAAAAAAGGATTACTATCCCTTGATGATACTATCATCTAGATGTGGAG	562
Oy	1018	GAAGTTCAGAAAGTATTGCTATACCGTATTGCACTGATTAATGCGCAATTGAACAACA	1077
Db	563	GTGACAAACAGCAGATAGATGAGAGGTGCCAACAGCTTAAAGATCAATTTACACAGCA	622
Oy	1078	CTTTCGACTTTGACCGGTGAATAACTCAAGAACCGTTGGCGAATTTACTGTTGTTGAG	1137
Db	623	CTGCTGTTTTCGACAAAGAAAGGCCCAAGACGCTTTATCTAAGTATCTGAGAGTGTG	682
Oy	1138	CTGTTATCAAAAGTAGAGCTCCAACAGACAGCTTTAAAAAGAAATGAACCTTGCAATTG	1197
Db	683	CTGTACTCAAGATTGGTGGAGCTAGTGAAGCTGAAGTGGTGTGAAAAAAATAGGGTTGA	742
Oy	1198	AGGATGCTCTTAAATGCTACACGTGCAGACCGTTGAAGAGATATCGTTGCTGGTGGAA	1257
Db	743	CAGATGCTCTTAAATGCTCAAGAGCGCTGCTGTGAGAGGCGCATTTGCCAGAGTGTGGAG	802
Oy	1258	CAGCACTTATTACGGTTATTGAANAAGTAGCAGCTCTTGAGCTTG---AGGCGATGATG	1314
Db	803	TTGCCCTTCTTTTTCGCACAGAGACCTTGACAGATTAACACAGCAAGAGACAGAGAA	862
Oy	1315	CTACTGACGTACATTTGTGCTTGCTGTCTGAGAAAGCCGTAGCTCAATTTGCTTTTA	1374
Db	863	ACATTGGAGTTCAAAATTTATCAAGAAATTTCTTGAAGCTCCCTTGATGACACATAGCTGAA	922
Oy	1375	ATGCTGGGTACGAAGGCTCCCTAGATTATTGACAAAGTTGA---AAACAGCGCTGCAGGAA	1431
Db	923	ATGCTGGCATTTGATGAGACCTTATGCTATGAGGAAGTCGATGACAAAGAGAGACCTCAATT	982
Oy	1432	CAGGATTTATGCTGCACAGAGTATGCGGTGATATGATTAATAACAGGATATGATGAC	1491
Db	983	TGGCGTATGATGAGCAAAAGAGGAGTACGTAGACATGATCAAGCGCGCATATGATGATC	1042
Oy	1492	CTGTCAAAAGTACAGATCAGCGCTTCAAAATGCAAGCTTCTGTAGCTATGCTTATTTTGA	1551
Db	1043	CGGTGAAGGTATTCGCAACGCGCATTTCAAGACGCTGCGAGATGTTTCCCTGCTATGCGAA	1102
Oy	1552	CACACGAAGCAGTTGTTGCTATTAATTAACGTGAAC	1585
Db	1103	CCACGGAGCGCTGCTGTCGACAGCTCCCGGCAAC	1136

RESULT 7				
AY108518	AY108518	1387 bp	mRNA	linear
LOCUS	Zetmays	PC0123570	mRNA sequence.	
DEFINITION	AY108518			
ACCESSION	AY108518.1	GI:21211596		
VERSION				
KEYWORDS	HTC.			
				HTC 25-MAY-2002

REFERENCE	AUTHORS	TITLE
JOURNAL	REFERENCE	Direct Submission
AUTHORS	TITLE	Submitted (25-Apr-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
JOURNAL	TITLE	Location/Outliers
FEATURES	source	1. 1387
		/organism="Zea mays"
		/db.xref="MaizeDB:637188"
		/db.xref="taxon:4577"
		/clone="PC0123570"
		/clone.lib="Maize Mapping Project/DuPont Consensus Library"
		/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
BASE COUNT	426 a	257 c 372 g 332 t
ORIGIN		
Query Match	17.5%	Score 290; DB 11; Length 1387;
Best Local Similarity	56.0%	Pred. No. 9.9e-70;
Matches 593; Conservative	0;	Mismatches 455; Indels 10; Gaps
Oy	568	TGAGAGTGTTGAAGCAGTCATTTGACCGGTGCTGCTCAATACATGTCGACAG 627
Db	14	TGAGATTGAAGAGGATGAGATTGACCGGGTTATTTCCCAATTTTGACAA 73
Oy	628	ACAAATGAAAAAGGTGTCACACCTTGGAACCCATTTATCTATACGAGATAAAAG 687
Db	74	ACCTGAGAAATGATTTGTGAGAGTTGAGAAATGTAAAGTTCTTTACGATCAGAAA 133
Oy	688	TCTCAACATCCCAAGACATTTTGCCACACTTTGAGAGAGTTCTTAAACCAACCGTCA 747
Db	134	TCAACAGCTAAAGAAATCTTCCATTTTGAGAAAGACACACAGCTGAGGCCCTC 193
Oy	748	TACGTATTATTCGACAGATGTGATGTGTAAGCACTTCCAAACCTTGTCTGAACAGA 807
Db	194	TCTTATTATTGTGAGACACTTACGTGGAAGGTTTGGCAACTTGTGTTAACAGC 253
Oy	808	TTCGTGTAATTTTCATGTGCTGCTGCTCAAGGCCAGAGTTTGTGATCGCTAAG 867
Db	254	TTTCGAGCAATTTCTCAATTTTGACGAGCTTAAGGCTCCAGTTTGTGAGACGGCGGAGG 313
Oy	868	CTATGCTTGAAGACATTTGCTTTCTTTCACAGGTGTACAGTAAATTCAGAGATAGAC 927
Db	314	CTGTACTTCAGACATTTCCATGCTCAGCAGGTGAGAGTTTCCCTACAAAAGATCTGGTT 373
Oy	928	TGAATTAAGAAGTCTCATATGACAGCCCTTTGAGACAGGCTGCTCAAGATTACAGTTGATA 987
Db	374	TCTTGTTGAATATCTCAGAGAGAACTTTGACACAGCAGAAAGTACAGATACATC 433
Oy	988	AAGATACACAGTAATTTGTGAAGGTTCAGAAATTCAGAACTATTTGTAACGTAATG 1047
Db	434	AACTACACAGACCTCATACAGATGACGCAATTAATTAATTAATTAATTAATTAATTA 493
Oy	1048	CAGTGATTAATGCAATTTGAACAACAACTTCTGACTTTGACCGGTGAAGAACTACAG 1107
Db	494	CACAACGAGAGAGAGCTTGAGACATGATTTAGTTATGATACAGAAATATGGCGG 553

Db 625 TTATTACCGACGCTAAATCTGTAAGTGGATTTTAAATAACCTTTGATCTTATGAGT 684
 Oy 678 GATAAAAAAGTGTCAACATCCAGACATTTTGGCCACTGTTAGAGAACTTTAAACC 737
 Db 685 GAAAGAGAGTCTCTCAATCCAGAGATATCTTCTTTGGAATTTGCAACCAACC 744
 Oy 738 AACCTTCATATCATTTATTTGAGATGATGATGAGAGCACTTCCACCCCTTCTC 797
 Db 745 AGAAGACCATTTGTTATCATTCGCCGAAAGATATATGATGCGG-ACITTTGGCTGCTGTAT 803
 Oy 798 TTGAACAGATTCCTGTACTTCAATGTGCTGCTGCAAGCCGAGATTGGTAT 857
 Db 804 TTGAACAGTGTGAGAGTCAAGTTTGTGCTGCTTAAAGCTCCAGCTTGGTAT 863

 RESULT 9
 BM799922
 LOCUS
 DEFINITION 1090 bp mRNA linear EST 05-MAR-2002
 AGENCOURT 6417164 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3492101
 VERSION
 BM799922
 SOURCE
 BM799922.1 GI:19116745
 EST.
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 1090)
 NIH-MGC http://mgi.mcl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-rt@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNL2113 row: k column: 14
 High quality sequence stop: 743.
 Location/Qualifiers
 1. 1090
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:3492101"
 /clone_id="NIH_MGC_67"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site: 1; Not; Site: 2; Salt; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Life Technologies."
 BASE COUNT 332 a 209 c 274 g 275 t
 ORIGIN
 Query Match 15 8% Score 262.8; DB 14; Length 1090;
 Best Local Similarity 56.2%; Pred. No. 3.6e-62;
 Matches 514; Conservative 0; Mismatches 337; Indels 3; Gaps 1;

Oy 198 GAAGATCATTTTGAACATGGAGCAAAATTTGTCTGAAGTGGCTTAAACCAT 257
 Db 302 AAGATTAATACAAAGAACATTTGAGCTAACTTTGCAAGTGTCCAAATACAAANT 361
 Oy 258 GATATTTGTGTGGAGAGCTACCTACCAAGTTTGAACAACCAATTTGCTATGAA 317
 Db 362 GAAGAGCTGGGGTGGACCTACCACTGCTACCTACCTACCTACCTACCTACCTAC 421
 Oy 318 GGACATAAAATTTGACACAGAGCTCAATACCAATTTGCTACCTACCTACCTAC 377
 Db 422 GCTTCGAGAAATTTGACAAAGCTCTATTCAGTGAATTCAGAGAGTGTATGTTA 481
 Oy 378 GCACAGCAACAGCTGTGAAGCCTTGAAGCCATTTGCTACCTGATCTGACAGAA 437
 Db 482 GCTGTGATGCTGTAATTTGTAAGCTTAAAGAGCTTAAAGCTTGAACCCCTGAA 541
 Oy 438 GCTATTTGCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 494
 Db 542 GAAATTTGCAAGGTTGCTACATTTCTGCAAGGAGCAAAAGAAATTTGCAATATC 601
 Oy 495 TCAGAGCTATGAGAGCTGTGGGCAAGATGTTGATATTCATGCAAGAAATTCGAG 554
 Db 602 TCTGATGCAATGAAAAAGTTGGAAGAGGTTGCTACATGATTAAGGATGAAAAA 661
 Oy 555 ATGGAACAGACTGAGAGTGTGAAGGCTGCAATTTGACCTGATGAGAGTCTGCTCA 614
 Db 662 CTGATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTC 721
 Oy 615 TCAATGCTAC 674
 Db 722 TACTTTATTAATCATCAAAAGGCTGCAAAATTTGCAAGAGCTGATGCTGTTG 781
 Oy 675 ACGGATTAATAAGTGTCAACATTCACAGATTTTGGCACTGAGAGAGTTCTTAA 734
 Db 782 AGTGAAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 841
 Oy 735 ACCAAGCTGCTATTCATTTATTTGATGATGATGATGATGATGATGATGATGAT 794
 Db 842 CACGCTAAGCTTTGCTATGATGATGATGATGATGATGATGATGATGATGATG 901
 Oy 795 GTCTTGAACAGATTTGCTGATTTCAATGATGATGATGATGATGATGATGATGAT 854
 Db 902 GTCTTGAATAGGCTTAAAGGCTGCTGCAAGGCTGCTGCAAGGCTGCTGCTGCT 961
 Oy 855 GATGCTGTAAAGCTATCTTGAAGACATTTGCTGATTTGCAAGGCTGCTGCTGCT 914
 Db 962 GACATTAAGAAAGACAGCTTAAAGATTTGCTGATTTGCTGATTTGCTGATTTG 1021
 Oy 915 GAGGATCTAGACT 928
 Db 1022 GAAAAAAGGCAATT 1035

 RESULT 10
 BM725584
 LOCUS
 DEFINITION 878 bp mRNA linear EST 07-MAR-2001
 GA_EB0024G33f Gossypium arboreum 7-10 dpa fiber library Gossypium
 arboreum cDNA clone GA_EB0024G33f, mRNA sequence.
 ACCESSION
 BM725584
 VERSION
 BM725584.1 GI:11206654
 KEYWORDS
 EST.
 SOURCE
 Gossypium arboreum.
 Gossypium arboreum.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
 REFERENCE
 1 (bases 1 to 878)
 Wang, R.A., Fitch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
 D., Wood, T.C., Leslie, A., and Wilkins, T.A.
 An integrated analysis of the genetics, development, and evolution
 of the cotton fiber
 Unpublished (2000)

Query Match	Score	DB	Length
Best Local Similarity	58.1%	Pred. No. 6e-62;	
Matches 458; Conservative	0;	Mismatches 330; Indels 0; Gaps	
481 TTGAGAGATATCTCAGAGCTGATGAGCGGTGGGCAAGATGGGTGATACATCG	540	11111	11111
28 TTGGAACATGATTTGCGTATGATTCAGAAAGTTGGACTGATGGTGTTCATCG	87	111111111	11111
541 AAGATCTCGAGATGAGAAACAACTGGAAGGTGTAAGGATGATTCACCGTG	600	11111	11111
88 AGTCATCTCCTATTGAGACCAAGTTGATGTTGAGAGAGATGAGATTCACAG	147	111111111	11111
601 GTTACCTGCTCATATGATGTCAGACATGAAATGTTGGACGCTTGAATACC	660	11111	11111
148 GTTACATCTCCCAATTTGATTAATACCGGAGAAATGTTGTTGAGTTTGAGAG	207	111111111	11111
661 CATTATCTTAACGAGGATGAAATGCTGCAAACTCCAGACATTTGCCACTCTG	720	111111111	11111
208 CAAAGATGTTGTAAGTATCAAAAGTTTACGATTTAAAGACATCATTCCTGTAG	267	111111111	11111
721 AAGAACTTTAAACCAACCGTCAATACATATTCAGATGATGATGATGAG	780	111111111	11111
268 AAGAAACCACTATTAAGATCTCTTCTTATTAATTCGAGAGATGATGAGAGG	327	111111111	11111
781 CACTTCCAACTCTTCTTGAACAGATTCGTGATCTTCATGTGTTCTGTAAG	840	111111111	11111
328 CTGCGCCACACTGTGTGGAACAACTGCTGTGCAATTCGATTCGACCACTTAAG	387	111111111	11111
841 CGCCAGATTTGTGATCGTGTAAAGCTATGCTTGAAGATGCTATCTTGCAGTG	900	111111111	11111
388 CTCTCTGTTTGTGAAGAGAAAGAAAGCTCTCTTCGATTAATTCGATTCGATG	447	111111111	11111
901 GTACAGTATTAACGAGACTGTAGACTGTGATTAAGAAATGCTACAAATGAC	960	111111111	11111
448 CTGAGTCCAGAGTACTGATTTGGGTGTTGCTGCGACGAAATCCTCAGTACG	507	111111111	11111
961 GACAGCTGCTAGATTAAGTTGATTAAGATTAACACATTAATTTGAGTGTAGGAA	1020	111111111	11111
508 GTATTCGCGAAGAGTGATCTTCCAGAGATGAGTCACTATTTGCTGACAGCC	567	111111111	11111
1021 GTTCAAGAGCTATGCTAAGCTTTGACGATTAATTCGATTAAGCAACACT	1080	111111111	11111
568 CAAGAGATGATATCAACACTGAGGTGCGCAACATTAAGAAAGACATCTGAC	627	111111111	11111
1081 CTGACTTTGACCGTGAAGAAATCAAGAACTTTGGCGAATTTAGTGTGTGTAGCT	1140	111111111	11111
628 CTGCTATGATTCGAAATTTGGCAAGAAAGATGCGCAACACTTCTGTGTGTGTG	687	111111111	11111
1141 TTATCAAGATGAGAGCTCCACAGACAGCTTTAAAGAAATGAACATTCGATGAG	1200	111111111	11111

Dd	688	TGATTAAGGTGGGGCTGCACAAAGACAGTACTGATGACTTCGTTACCTTGCGATTAG	747
Oy	1201	ATGCCCTAATGCTACAGTCAGCCGCTGAAGAAGCTGCTGCTGCGTCGACAG	1260
Dd	748	ATGCAAGAATGCTACATTTCCTGCGCATGAGAGATATTCCTGCTGAGTGGCTG	807
Oy	1261	CACCTATT	1268
Dd	808	CCTTAGIT	815
RESULT 11			
Locus	AL518632		
DEFINITION	AL518632 LTR_NFL011.NBCI Homo sapiens cDNA clone CSDBA009Y115	1035 bp	mRNA linear EST 13-FEB-2001
ACCESSION	AL518632		
VERSION	AL518632.1		
KEYWORDS	GI:12782125		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
ATTORNS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
JOURNAL	1.(bases 1 to 1035)		
COMMENT	Li,W.B., Gruber,C., Jessee,J. and Polayars,D. Full-length cDNA libraries and normalization unpublished (2001) Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91005 Evry cedex - France Email: seqef@genoscope.cns.fr, Web : www.genoscope.cns.fr.		
FEATURES			
source	Location/Organisms		
	1..1035		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="CSDBA009Y115"		
	/clone_id="LTR_NFL011.NBCI"		
	/sex="male"		
	/tissue_type="neuroblastoma cells"		
	/lab_host="DH10B"		
	/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliangellife@tech.com URL : http://fulllength.invitrogen.com"		
BASE COUNT	311 a	195 c	259 g 266 t 4 others :
Query Match	15.5%	Score 257.2	DB 9; Length 1035;
Best Local Similarity	56.3%	Pred. No. 1.3e-60;	
Matches 500;	Conservative 1;	Mismatches 384;	Indels 3; Gaps 1;
Oy	18	GCAAAAGAACATCAATTTTCAGAGATGCGGTGCGCAGTGGCGCGAGTTGATG	77
Dd	116	GCACAAGATGATAAATTGGTGGAGATGCCGAGCCTTAATGCTTACAGTGNACCTT	175
Oy	78	TTAGCAATGCGCTGAAGACGCTTGCTGCTTAAGAGCCCATGTTGCTGTAAAAA	137
Dd	176	TTAGCCATGCTGTGCGCGCTTACATATGGGCGCAAGAGAAACAGATGATTATGACG	235
Oy	138	GCTTTTGCTTCCTTAATTAAGATGCGGTACACCTGCTTAAGATGATGATTA	197
Dd	236	ACTGTGGGAGTCCCAAGTAAACAAAGATGCTGATCGTTGCAAAAGTCAATTAACCTA	295
Oy	198	GAAATCATTTTGAANAACATGGAGCAAAATTTGCTTCTGAAATGCGCTTCAAACCAAT	257

Db 296 AAGATTAATACAAAAACATTGAGCTAACTGTTCAGATGTTGCCATACACAAAT 355
OY 258 GATATGCTGGTGGAGGAGGAGTACATGACACATTTGACACAAAGCATTTGTCATGA 317
Db 356 GAGAAAGCTGGGAGTGGACCTACCTACTGCTCTACTGACAGCTCTATGACAAAGAA 415
OY 318 GGACTAAAAATGTCACAGAGCTGTATCCAAATTTGATCTCGTACAGGACATGAACA 377
Db 416 GGCTTGAGAGATTTAGCAAGAGTGTCTATCCAGTGAATACGAGAGAGTGTATGTTA 475
OY 378 GCAACAGCAACAGCTGTGAAAGCCATTGCTCAACCTGATCTGCAAGAA 437
Db 476 GCTGTTGATGCTGTAAATTTGCTGAACTTAAAGAGAGCTGAAACCTGACCCCTGAA 535
OY 438 GCTATGCTGAGTCTGCTGAGTATCATCAGCTGCAAGAAAG--TTGGAGAGTATTC 494
Db 536 GAAATTCACAGGTTGCTACGATTTCTGCAAGAGAGACAAAGAAATTTGCCAATTCATC 595
OY 495 TCAGAGCTATGAGAGCTGTGGCAACGATGTTGATTCATCCATGCAAGAACTCGAGGT 554
Db 596 TGTGATGCAATGAAAAAGTTGAGAGAAAGGCTGTCTACACAGTAAAGATGAGAAACA 655
OY 555 ATGGAACAGCACTTGAAGAGTGTGAAGAGTGTGACCTGCTTACCTGCTCA 614
Db 656 CTGAATGATGAAATTAAGATTTATGAGAGGAGTGTGATGAGAGCTGATTTCTTCA 715
OY 615 TACATGCTGACAGCAATGAAAAATGTTGCAAGCTTGAAGAAACCATTTATCTTAATC 674
Db 716 TACTTATTAATACATCAAGAGTCAAGAAATGTAATTCAGAGTGTCTGTTCTGTTG 775
OY 675 ACGATTAATAAAAGTGTCAAAATCCAAACATTTTCCACTACTGAGAGATTTCTTAA 734
Db 776 AGTGAAGAAAAATTTCTAGTATCCAGTCAATGTCCTGCTGCTTGAATTCGAATGCT 835
OY 735 ACCAACCTGCTACTACTATTTATGAGATGATGATGATGATGATGATGATGATGAT 794
Db 836 CACCGTAAGCTTTGCTGATTAATCCCTGAGATGTTGAGAGAGAGCTGATGATGATG 895
OY 795 GCTTGAACAGATTTGCTGATCTTTCAATGTTGTTGCTGCTGCTGCTGCTGCTGCTG 854
Db 896 GCTTGAATAGCTAAAGAGTGTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 955
OY 855 GATCGTGAAGCTATGCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 902
Db 956 TGACATATGATAGAGAGCTTAAAGATTTGCTATGCTGCTGCTGCTGCTGCTGCTG 1003

RESULT 12
LOCUS BG321293 977 bp mRNA linear EST 27-FEB-2001
DEFINITION Zm04_04909.R Zm04_AAPC_ECORC_cold_stressed_maize_seedlings Zea mays
ACCESSION BG321293
VERSION BG321293.1 GI:13150971
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 977)
AUTHORS Singh, J.A., Makul, K., Courroux, P., De Moors, A., Harris, L.J., Hattori,
J.I., Ouellet, T., Robert, L.S., Sprout, D. and Tinker, N.A.
TITLE Expressed Sequence Tags from Cold-Stressed Maize Seedlings
JOURNAL Unpublished (2001)
COMMENT Contact: Singh, J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-Food Canada
KW Nealey Bldg., Central Experimental Farm, Ottawa, Ontario, KIA
OC6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.

FEATURES
source Location/Qualifiers
1..977
/organism="Zea mays"
/cultivar="CO328"
/db_xref="taxon:4577"
/clone="Zm04_04909"
/clone_id="Zm04_AAPC_ECORC_cold_stressed_maize_seedlings"
/issue="leaf, crown"
/note="Vector: Bluescript SK-/XhoI-EcoRI; Site_1: Eco RI;
Site_2: Xho I; Lower temperature 50 C / hour from 22 to
120C; bring to 50 in 1 hour from 120C. Leave at 50C 2 days
photoperiod 16 hours. Light intensity was 125 ue-1.
Library prepared by in vivo mass excision from amplified
library"
BASE COUNT 276 a 205 c 241 g 223 t 32 others
ORIGIN
Query Match 15.38; Score 254; DB 12; Length 977;
Best Local Similarity 56.78; Pred. No. 9.8e-60;
Matches 440; Conservative 23; Mismatches 310; Indels 3; Gaps 1;
OY 7 GCCTTCATATGCGAAAGAAATCAAAATTTTCAGCAGATGCGCTGCTCCATGTCGCG 66
Db 202 GGAAATGCGCGGAGAGACATCAAGTTGTTGAGAGCGCCGTTCTCTATGTTGAAG 261
OY 67 GAGTGAATATGTAGACATACCGTCAAGTAAAGTGTGCTGCTTAAAGGCGCATGTTG 126
Db 262 GTGTTGAGAGGTTGGCAGAGCTTTAAAGTTAAATGAGCTTAAGGCGCGCATGTTG 321
OY 127 TCTTGAAGAGCTTTTGTCTCCCTTAATTAATGAGAGGCTTAACCTATGCTTAAG 186
Db 322 TTATGAGCAACCTTTGCTGCAACCAAGTACAAAGATGTTGCTTGAACAAAGA 381
OY 187 AGATGGAATTAAGATCATTTTGAAGACAGAGCAAAATTTGCTGTAAGTGGCTT 246
Db 382 GCATTAATTTAAGATAGATTAAGAAATGTTGGCAACCTGTGTAAGACAGTGTGTA 441
OY 247 CTAAACCAATGATTTGCTGTGATGAGAGCACTACTGCACAGTGTGACAAAGCA 306
Db 442 ATGCAATTAAGATAGATTAAGAAATGTTGGCAACCTGTGTAAGACAGTGTGTA 441
OY 442 ATGCAATTAAGATAGATTAAGAAATGTTGGCAACCTGTGTAAGACAGTGTGTA 501
OY 307 TTGTCATGAGAGCTAAAAATGTGACAGAGTGTGTAATTCATTTGATTCCTGAG 366
Db 502 TATTTACTGAGGAGTGCAGAAATCTGTCGCGCTGGAATKATGCTATGATTTAAGCG 561
OY 367 GCATTTGAACAGCAACAGCAACAGCTGTGAAGCTTGAAGCACTTGCATCACTGTAT 426
Db 562 GAAACTCAATGCTGTGAGCGCTGTTTACCAATCTTAAAGATGAGCCAGATATATCA 621
OY 427 CTGCAAGAGAGCTTTGCTCAGTGTGCTGAGTATGATCAGCTGTGAAG--AAGTTG 483
Db 622 GCATTCAGAGAAATTCACAGAGTGTGATGATGATGATGATGATGATGATGATG 681
OY 484 GAGAGTAAATTCACAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 543
Db 682 GTGAGCTATGCTCAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 741
OY 544 AATTCAGAGTATGCAAGCAAGTGAAGTGTGATGATGATGATGATGATGATGATGAT 603
Db 742 ACGTGAACACCTTTATTAATGATGATGATGATGATGATGATGATGATGATGATG 801
OY 604 ACGTGTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 663
Db 802 ACATCTCTCCGATCTTCAATTCACCAACCAACCAACCAACCAACCAACCAACCAAC 861
OY 664 TTATCTTAATCAAGGATTAAGTGTCAACATCAAGCAATTTTGGCACTGCTGAGG 723
Db 862 TGATCTTAATCAAGGATTAAGTGTCAACATCAAGCAATTTTGGCACTGCTGAGG 921
OY 724 AAGTCTTAACCAAGGCTCATTTACTATGATGATGATGATGATGATGATGATGATG 779
Db 922 TGGCTCTTAAGAAACAAAGCTCTGCTGATTTTTCAGAGAGAGTGAAGTTAA 977

```

RESULT 13
AL532233      988 bp      mRNA      linear      EST 13-FEB-2001
LOCUS         AL532233 LFI_NFL001_NBC4 Homo sapiens cDNA clone CS0DM004YH20 5
DEFINITION    prime, mRNA sequence.
ACCESSION     AL532233
VERSION       AL532233.1 GI:12795726
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 988)
AUTHORS       Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE         Full-length cDNA libraries and normalization
JOURNAL       Unpublished (2001)
COMMENT       Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 Evry cedex - France
               Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..988
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CS0DM004YH20"
/clone_lib="LFI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/label="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@litech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT    306 a      188 c      242 g      251 t      1 others

Query Match      15.3%; Score 253.4; DB 9; Length 988;
Best Local Similarity 57.1%; Pred. No. 1.5e-59;
Matches 500; Conservative 0; Mismatches 371; Indels 4; Gaps 2;

OY 18 GCAGAAAGATCAATTTTCAGAGATGGCGCTGCCATGCGCCGCGAGTTGATG 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 115 GCCAAATATTAATTTGGTGCAGATGCCGAGCTTAATCTCAAGGTAGCCTT 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 78 TTACCAATACCGTCAAGTACGCTTGCCTTAAGGGCGCATGTTCTTGAAAA 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 175 TTACGCGATGCTGTGCGCTTACATGGGGCCAAAGGAAGCATGATTATGACAG 234
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 138 GCTTTGTTCTCCCTTAATTAATGAGGGGTAAACCATTTGTAAGAGATCAATTA 197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 235 AGTTGGGAGTCCCAAGTACAAAGATGGTGTGCTGCAAGTCAATGACTTA 294
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 198 GAAGATCAATTTGAACATGGAGGCAAAATGTTGCTGAAGTGGCTTCAAAACAT 257
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 295 AAAATATTAATCAAAACATTTGAGAGTCAACTTTCAGATGTTGCCAATACAAAT 354
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 258 GATATTCGTGTGATGAGCACTACTGCAACAGTTTGACACAAAGCATTTGTAAGA 317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 355 GAAGAACTGGGATGAGCACTACTGCTACTGTGACAGCGCTCTATAGCAAGAA 414
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 318 GAGCTAAATAATGTGACAGAGTGTATCATCATTTGATGAGTGTGTAAGCA 377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 415 GGCTTCAGAGAAATTAGCAAAAGGTGCTAATCATGTAAGAGAGGTGATGATTA 474
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 378 GCACACACAAAGCTGTGAAGCTTGAAGACCATTTGCTCAACCTGATTTGGCAAGAA 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

DB 475 GCTGTGATGCTGTATATGCTGAACTTAAGAAAGCAGTCAACCTGTGACCAACCCCGA 534
OY 438 GCAATTCGTCAGGTCGCTGAGTATCATCATCGTCTGAAAAG---TTCAGAGATATATG 494
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 535 GAATTTGCACAGGTTGCTACATTTCTGCAAACGAGACAAAGAAATTTGGCAATATCATC 594
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 495 TCAGAGCATATGAGCGGTGTGGCAACGATGCTGATTTACATCAAGAAATCTCGAGGT 554
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 595 TCTGATGCAATGAAGAAAGAGTGAAGAAAGGCTGATCAACAGTAAGAAATGAGAAAGAA 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 555 ATGGAACAGAACTTAAGTGGTTGAAGGATGCAATTTGACCGTGGTACCTGTCAAA 614
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 655 CTGAATGATGATTAAGAAATTTGAAGGATGAAGTTGATGAGCTATATTTCTCCCA 714
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 615 TACATGTCACAGCAATGAAGAAATGTTGACAGCTTGAAACCATTTTCTTAATC 674
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 715 TACTTATTATACATCAAGTACAGAAATGGAATTCAGATGCTATGTTCTGTG 774
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 675 ACGGATTAAGAAAGTGCACAACTCCAGACATTTGACACTGATGAGAAAGTTCTTAAG 734
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 775 AGTGAAGAAAGAAATTTCTGATTCACATGCTATGCTGCTTGAATTTGCAATGCT 834
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 735 ACCAACGCTCATTTACTCATTTATTCAGATGATGATGATGATGATGATGATGATGATGAT 794
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 835 CACCGATAGCGCTTTGGCTATATATCGTGAAGATGTTGATGAGAGCTTAAATGATCACTC 894
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 795 GCTGTGACAAAGTTCGTGCTACTTTCATGCTGCTGCTGCTGCAACCGCAGATTTGCT 854
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 895 GTCTTAATAGCTTAAGATTTGCTCTTCAGGTGTGCGACGACGACGCTCCAGGCTCAGGTT 954
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 855 GATCGTCAATAGCTATGCTTGAAGACATTTGCTAT 889
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 955 GACAAATAG-AAAGACAGCTTAAGAAATATGCTAT 988
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
AL515262      955 bp      mRNA      linear      EST 13-FEB-2001
LOCUS         AL515262 LFI_NFL006_PU2 Homo sapiens cDNA clone CLOB016ZA04 5
DEFINITION    prime, mRNA sequence.
ACCESSION     AL515262
VERSION       AL515262.1 GI:12778755
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 955)
AUTHORS       Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE         Full-length cDNA libraries and normalization
JOURNAL       Unpublished (2001)
COMMENT       Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 Evry cedex - France
               Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..955
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CLOB016ZA04"
/clone_lib="LFI_NFL006_PU2"
/tissue_type="placenta"
/notes="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@litech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT    288 a      181 c      236 g      247 t      3 others

```

Wed Apr 16 08:05:37 2003

us-09-001-737-7.rst

Page 13

ORIGIN

Query Match 15.18; Score 251.6; DB 9; Length 955;
Best Local Similarity 57.08; Pred. No. 4.6e-59;
Matches 480; Conservative 0; Mismatches 359; Indels 3; Gaps 1;

18 GCAAGAGAAATTCATTTTTCAGAGATGCGCTGCGCATGCGCGGAGTGAATG 77
114 GCCAAGATTAATTAATTTGGCGAGATGCCAGGCTTAATCTTCAAGGCTGACCTT 173
78 TTACAGATACGCTCAAGATTAAGCTTGGCTTAAGGCGCAATGTTCTTGAAGAA 137
174 TTAGCCATGCTGCGCTTACAAAGGCGCAAGGAAAGAAAGATATTATGAGCAG 233
138 GCTTTGCTTCCCTTAATTAATGAGGGGTAACATTTGCTTAAGAGATGAATTA 197
234 AGTGGGGAAGTCCCAAGTAAGATGCTGACTTTGCAAACTCAATGACTTA 293
198 GAAGATCATTTTGAACATGAGCAAAATGCTGCTGAAGTGGCTTCAAAACCAT 257
294 AAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 353
258 GATATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 317
354 GAAGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 413
318 GGACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 377
414 GCTTGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 473
378 GCAACAGCAAGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 437
474 GCTGTTATGCTGCTTATGCTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 533
438 GCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 494
534 GAATTTGCAAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
495 TCAGAACTATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 554
594 TCTGATGCTATGAAGAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
555 ATGGAAGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 614
654 CTGAATGATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 713
615 TACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 674
714 TACTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 773
675 ACGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 734
774 AGTGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 833
735 ACGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 794
834 CACGCTAAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 893
795 GCTTGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 854
894 GCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 953
855 GA 856
954 GA 955

RESULT 15
AL515579
LOCUS
DEFINITION AL515579 LTL_NFL011_NBC1 Homo sapiens cDNA clone CS04A002YD20 5
PRIMER, mRNA sequence.
ACCESSION AL515579

VERSION
EST
SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

BASE COUNT

ORIGIN

Query Match 15.08; Score 249.6; DB 9; Length 1017;
Best Local Similarity 56.88; Pred. No. 1.7e-38;
Matches 478; Conservative 1; Mismatches 360; Indels 3; Gaps 1;
18 GCAAGAAATTCATTTTTCAGAGATGCGCTGCGCATGCGCGGAGTGAATG 77
116 GCCAAGATTAATTAATTTGGCGAGATGCCAGGCTTAATCTCAAGGCTGAGACCTT 175
78 TTACAGATACGCTCAAGATTAAGCTTGGCTTAAGGCGCAATGTTCTTGAAGAA 137
176 TTAGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 235
138 GCTTTGCTTCCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 197
236 AGTGGGGAAGTCCCAAGTAAGAAAGATGAGTGAATGCTGCAAGCAATTAATTAAT 295
198 GAAGATCATTTTGAACATGAGCAAAATGCTGCTGAAGTGGCTTCAAAACCAT 257
296 AAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 355
258 GATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 317
356 GAAGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 415
318 GCACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 377
416 GCTTGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 475
378 GCAACAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 437
476 GCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 535
438 GCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 494
536 GAATTTGCAAGAGGCTTACGATTTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 595

```
OY 495 TCAGAACCTATGAGCGTGTGGCAGACGATGTGATTACCATCGAAGAACTCGAGGT 554
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 596 TCTATGCAATGAAAAAGTTGGAGAAAGGCTGTCTACACAGTAAAGATGAAAAACA 655
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 555 ATGGAACGAGACTYGAAGTGTGAGAGCATGCAATTGACCGTGGTACCTGTCTCAA 614
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 656 CTGAATGATGAATTTAGAAATTATTGAGAGCATGAGTTGATCGAGGCTATATTCTCCA 715
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 615 TACATGGTCACAGCAATGAAAAATGGTTGCAGACCTTGAAACCATTATCTTAATC 674
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 716 TACTTATTAAATACATCAAAAGGTCGAAATGTGAATTCAGATGCGCTATGTCTGTG 775
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 675 ACGGATAAAAAAGTCAAAACATCCAAAGACATTTGCCACTACTTGAAGAACTTCTTAA 734
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 776 AGTGAAGAAAGAAATTTCTAGTATCCAGTCGCTGTGACCTCTTGAAATTCGCAATGCT 835
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 735 ACCAACCCTCATACATCATATATGCAATGATGTGATGGTGAAGCACTTCCAAACCTT 794
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 836 CACCGTAACCTTTGTCTATATCCCTGAGAGATGTGATGAGAGGCTCTAAGTACACTC 895
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 795 GTCTTGAACAGATTCTGTGACTTTCATATGTGTGCTGTCAAAGGCCAGGATTTGGT 854
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 896 GTCTTGAATAGCTTAAGGTTGGTCTTCAAGTTGTGCGAGTAAAGGCTCCAGGTTTGGT 955
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 855 GA 856
    |||||
Db 956 GA 957
    |||||
```

Search completed: April 15, 2003, 04:19:17
Job time : 2499.54 secs